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Title:
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Sequence:
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              score:
  US-09-897-645-1
618
1 MRMIVGHGIDIEEI
                                                                               December 10,
                                                                              2003,
                                                                                19:30:51
                                                    .; Search time 41 Seconds (without alignments) 472.308 Million cell updates/sec
   . ISHTDQFVTASVILEENHES
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Scoring table:
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Searched: 1107863 seqs, 158726573 residues

Total number O M hits satisfying chosen parameters: 1107863

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Minimum
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length:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s Maximum Listing

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Database
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A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

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6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

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11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

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21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

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Pred. No. is the number of score greater than or equal and is derived by analysis number of results 1 or equal to the analysis of the t s predicted by chance to have a e score of the result being printed, total score distribution.

SUMMARIES

i	Score	30	Leng	i U	ID	Description
י בי	618	100.0	122	19	AAW80612	s. pneumo
2	618	00.	122	22	AAU37879	Streptococcus pneu
ω	618	00.	122	22	AAU38056	Streptococcus pneu
4	\vdash	100.0	156	21	AAY88388	S-ydcB essential b
ហ	O	8	120	21	AAY58607	Streptococcus pneu
Q	608	98.4	120	24	ABU02175	S. pneumoniae type
7	w	4.	118	23	ABP27226	Streptococcus poly
80	28.	ω ·	119	21	AAY91289	Group B Streptococ
9	328.5	53.2	119	23	ABP27225	Streptococcus poly

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222 222 222 222 222 223 223 234 245 246 246 256 256 256 256 257 257 257 257 257 257 257 257 257 257	88000C44WG4
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11	22 22 22 22 22 22 22 22 22 22 22 22 22
AAW16453 AAU34663 AAU34663 AAU346126 AAY34912 ABP80377 AAU54107 AAU54107 AAU35774 AABB08801 ABB08801 ABB08805 ABB08806 ABB08806 ABB08807 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481 AAG92481	383518 5213 75213 7563 7563 7563 7563 7563 7563 7563 756
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ALIGNMENTS

Ø tandard; Protein; 122 **A**

AAW80612;

24-DEC-1998 (first entry)

pneumoniae protein of unknown function.

Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment; hypothetical; cell wall biosynthetic, external target; minimal gene set protein.

Streptococcus pneumoniae.

WO9826072-A1.

18-JUN-1998.

09-DEC-1997; 97WO-US22578.

13-DEC-1996; 96US-0036281.

) LILLY & CO ELI.

RESULT 1
AAW80612
ID AAW80612;
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AC AAW80612;
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DT 24-DEC-19:
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DE S. pneumon
XX
Cell wall
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OS Streptocoo
XX
PN WO9826072
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PF 09-DEC-19:
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PF 13-DEC-19:
XX
PI Baltz RH,
PI Skatrud PI
PI Young Bell
XX Baltz RH, Mills BJ, Skatrud PL, Young Belli Bellido ML; Burgett SG, Dehoff BS, Norris FH, Peery RB, Smith MC, Solenberg Dehoff BS, Hoskins JA, Jaskunas SR; eery RB, Rockey PK, Rosteck PR; Solenberg PJ, Treadway PJ;

1998

348529/30

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RESULT 2
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ID AAU3
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Matches 122
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
23-OCV-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical, cell wall biosynthetic, external target, or minimal gene set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of proteins. The invention also provides a DNA chip having arrayed on it least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 177; 333pp; English.
                                                                                                                                                                                                   WO200170955-A2.
                                                                                                                                                                                                                           Streptococcus pneumoniae
                                                                                                                                                                                                                                                       antibiotic;
                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae cellular proliferation protein
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                                                                                                                                              21-MAR-2001;
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             (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also be used to detect S. pneumoniae cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion. The invention provides DNA sequences (AAV65201 to AAV65304) the Streptococcus pneumoniae genome and corresponding protein inces (AAW80605 to AAW80728). The protein sequences are classified hetical, cell wall biosynthetic, external target, or minimal generateins. A recombinant host contains.
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122; Conservative (
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                                    2000US-191078P.

2000US-206848P.

2000US-207727P.

2000US-242578P.

2000US-253625P.

2000US-257931P.

2000US-269308P.
                                                                                                                                                                                                                                                       antibacterial; drug
                                                                                                                                               2001WO-US09180.
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Pred. No. 2.7
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n of virulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes, their use in the agenes themselves and the Escherichia coli, Staphy
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   21-MAR-2000
23-MAY-2000
                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2002
                                                                                                                                                                                                                                              Streptococcus pneumoniae.
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 2000US-191078P.
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery corgrammes. The antisense nucleic acid sequence for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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Yamamoto R
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                                                                 Bacteria; S-ydcB; Streptococcus acyl carrier protein synthase;
                        Streptococcus
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11 Similarity 100

122; Conservative
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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Pred.
                                                                   identify; ba
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red. No. 2.7
Mismatches
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cterial infection;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the protein encoded by the essential bacterial gene S-ydcB from Streptococcus pneumoniae. B-ydcB is an S-ydcB ortholog from Bacillus subtilis. The gene encodes a a protein which has structural characteristics of acyl carrier protein synthase and displays synthase activity in vitro. The protein is used in a method for identifying an antibacterial agent, which comprises contacting an S-ydcB or B-ydcB polypeptide with a test compound and detecting an interaction between the polypeptide and the test compound, where the interaction indicates that the compound is an antibacterial compound. Antibacterial agents identified using the method may be used to treat a bacterial infection, especially Streptococcus pneumoniae in mammals, especially a human or rodent. The method can be configured for high throughput screening of numerous candidate antibacterial agents, and identified agents should have a broad spectrum of antibacterial activity.
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N-PSI
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                                                                               Acyl
diag
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polypeptide
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                                                     Streptoco
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                                                                                                                                               11-APR-20
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AA13270.
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                                                                              er protein synthase; acpS; infection; therapy; antibacterial; antibiotic; Helicobacter pylori
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                                                                                                                                                (first entry)
                                                                                                                       pneumoniae acyl carrier
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                                                                                                                                                                                                    Protein;
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                                                                                                                       protein synthase acpS
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Matches 120
                                                                                                                                                                                                                                                                                                                             prevent, inhib can also be us pneumonia, bac endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 having at least 70% identity with the present sequence, as acps polynucleotides, recombinant materials and methods for production. The polypeptides and polynucleotides can be us the diagnosis, prognosis or treatment of a disease related expression or activity of acps. They can be used to treat diseases such as bacterial infections, particularly S. pneu infections, to prevent infections and to identify agonists antagonists useful as antibacterial compounds. They can always to prevent bacterial adhesion to mammalian, extracelly
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N-PSDB; AAZ35350.
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          Bacterial meningitis; pneumonia; ear infection; antiinflammatory; auditory; respiratory; gene ther
                                                                                                                                                                                                                                                                           Sequence
                                                                    11-FEB-2003
                                                                                       ABU02175
                                                                                                         ABU02175
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                                                pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lated Streptococcus pneumoniae products for treating, e.g. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SC,
                                                                                                                                                                                                                                      n 98.4%;
Similarity 100.0%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 31-32;
                                                                                                                                                                                                MIVGHGIDIEELASIESAVTRHEGFAKRVLTAQEMERFTSLKGRRQIEYLAGRWSAKEAF
                                                                                                                                                                                                                                                                                                        ed cancers, such as gastrointestinal carcinoma, and also to inhibit and/or cure gastric ulcers and gastritis. They be used for treating e.g. otitis media, conjunctivitis, bacteraemia, meningitis, sinusitis, pleural empyema and
                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                             120 AA;
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Pred. No.
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                    sepsis; otitis antibacterial;
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93 (NCIMB 40794), which is
of the acyl carrier protein
ides acpS polypeptides having
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3-68;
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                    media;
                                                region
                                                                                                                                                                                                                                                         Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be used for related to the
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                     stimulant
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Matches 120
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N-PSDB; AI
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                                                                                                                                                                                                                                                                                                              medicaments for treating or preventing a disease or infection due streptococcus bacteria, particularly S. pneumoniae, such as pneumoses, otitis media or ear infection. They are also useful in devaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one the 2469 proteins expressed by the identified coding regions from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or ear
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                                                                                                                                                                                                                             Note: The sequence data for this patent did not form of the printed specification, but was obtained in eleformat directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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                                                               SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ins and nucleic acid molecules from Streptococcus pneumoniae, medicaments for treating or preventing a disease or infection reptococcus bacteria, such as pneumonia, sepsis, otitis media
01; 2001GB-0007658
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                       The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                      Query Match
Best Local S
Matches 62
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24-NOV-2000;
07-MAR-2001;
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N-PSDB; ABN67857.
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                                                  63
                                                                                                                                                                      Similarity 53.4%; 62; Conservative
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2001GB-0005640.
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7; Mismatches
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larity 52.1%;
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99US-0125163.
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                                                                                                                                                                                         119 AA.
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Pred. No. 5.3e-33;
Pred. No. 5.3e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity contactions of the distinguishing/identifying
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24-NOV-2000;
07-MAR-2001;
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antiinflammatory; infe
                                                                                                                                               ABB5
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N-PSDB; ABN67856.
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                         Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Streptococcus proteins
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                                                                  6-MAY-2002
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57
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disease caused by Streptococcus bacteria, su
captured that binds to the protein of the protein 
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INST GENOMIC
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                                                                                                                                                  standard;
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2000GB-0028727.
2001GB-0005640.
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                       protein
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fection; v
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52.1%;
tive 2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 328.5; DB 23 Pred. No. 5.3e-33; Mismatches 26;
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such as me
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Indel
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RESULT 11
AAU35183
ID AAU35
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AC AAU35
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DT 13-FE
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KW Antik
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in th production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New
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 21-MAR-20
23-MAY-20
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                  Antisense; | antibiotic;
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                                                     27-SEP-2001.
                                                                           WO2001709
                                                                                              Enterococcus faecalis
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                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                    prokaryotic
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larity 51.3%;
Conservative 25
                                                                                                                   antibacterial; drug
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 2000US-191078P.
2000US-206848P.
                                 2001WO-US09180
                                                                                                                                                   faecalis
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Pred. No. 1.1e-29;
25; Mismatches 31;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins.

The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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N-PSDB;
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                                                                                                                 Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published
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Pred. No. 1.5e-29;
Mismatches 35;
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N-PSDB; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae. The gene encodes a protein which has structural characteristics of acyl carrier protein synthase and displays synthase activity in vitro. The protein is used in a method for identifying an antibacterial agent, which comprises contacting an S-ydcB or B-ydcB polypeptide with a test compound and detecting an interaction between polypeptide and the test compound, where the interaction indicates that the compound is an antibacterial compound. Antibacterial agents identified using the method may be used to treat a bacterial infection especially Streptococcus pneumoniae in mammals, especially a human or rodent. The method can be configured for high throughput screening of numerous candidate antibacterial agents, and identified agents should have a broad spectrum of antibacterial activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying new antibacterial agents particularly against Streptococcus pneumoniae, uses S-ydcB polypeptide from S. pneumoniae and B-ydcB polypeptide from Bacillus subtilis -
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DE Listeria
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, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
ty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
ty T, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
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g ÃÕ g Š Search completed: December Job time : 42 secs The present invention relates to the genome sequence of Listeria C monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. C monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein c encoded by the genome sequence of the present invention. Proteins c expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and c for biosynthesis and biodegradation, especially biosynthesis of Vitamin C B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. Mote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences. Query Match Best Local S Matches 50 Sequence <u>.</u> و 13 th 37.7%; Similarity 42.7%; 50; Conservative 3 \vdash || | |:|: :| :: | :: | :|||| :|:::| :| |:||||:|||:|||:|||:||||: MIVGHGIDIEELASIESAVTRHEGFAKRVLTAQEMERFTSLKGRRQIEYLAGRWSAKEAF 62 SEQ 118 AA; ID No 286; 10, 192pp; 2003, Score 233; DB 2; Pred. No. 5e-21; 30; Mismatches French. 19:35:09 23; 35; Length 118; Indels part of the printed directly from WIPO infections by L 2. Gaps 60 and Ľ ĝ 2:

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RESULT 3
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; Sequence 6990, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm a
; TITLE OF INVENTION: NUCLEIC ACID AN
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APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF S-YDCB AND B-YDCI
FILE REFERENCE: 07334/097001
CURRENT APPLICATION NUMBER: US/09/163,446
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
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Best Local Similarity 100.0%;
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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09-163-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
TYPE: PR
        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
FILING DA
                                                                                                                                                  ZIP: 02354
COMPUTER READABLE
MEDIUM TYPE:
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INFORMATION:
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CITY: Waltham
STATE: Massachusetts
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                                                                                                                         SYSTEM:
E: July 2, 1 INFORMATION:
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                                                                                                                                                              FORM:
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          1998
60/051571
2, 1997
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                                                                                                                                                                                                                              Street
                                                                                    US/09/107,532A
                                              60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618; DB 4;
Pred. No. 9.6e-71;
Mismatches 0;
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AND AMINO ACID S
FAECIUM FOR DIAG
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                                                                                                                                                                                                                                          CORPORATION
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RESULT 5
US-09-134-001C
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US-09-163-446-
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LOCATION: (B) LOCATION 1...129
SEQUENCE DESCRIPTION: SEQ ID NO: 6990:
US-09-107-532A-6990
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                                                                                                                                                                                                                                                                                    US-09-163-446
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF S-YDCB AN
FILE REFERENCE: 07334/097001
CURRENT APPLICATION NUMBER: US/09/16
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Versic
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APPLICANT:
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Best Local S
Matches 54
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Best Local S
Matches 56
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                              LENGTH: 12
TYPE: PRT
ORGANISM:
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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No. 6515119
INFORMATION:
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CULE TYPE: protein
THETICAL: YES
                                                                                                                                                                                                                         40.6%; Score 251; DB 4; I imilarity 44.6%; Pred. No. 3.2e-24; Conservative 25; Mismatches 32;
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SKAFGTGIGRQLSFQDIEIRKDQNGKPYIICTKLSQA--
                                                                                                                                                                    Streptococcus pneumonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 129 amino TYPE: amino acid
                                                                                                                                        SKAMGTGISK-LGFODLEVLNNERGAPY--
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ilarity 48.3%;
Conservative 21
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; Pred. No. 5.1e-29;
21; Mismatches 39;
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                                                                                                                                       -- FSQAPFSGKIWLSISHTDQFVTASVIL
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                                                                                                                                                                                                                                                     Length 121;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-728-742A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10, ...; Sequence 10, ...; Patent No. 6579695; Patent INFORMATION: Ralph H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4274, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM:
                                                                                              APPLICATION NUMBER: US/08, FILING DATE: October 11, PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/00: FILING DATE: October 13, APPLICATION NUMBER: 60/02: FILING DATE: July 12, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q ID NO 4274
LENGTH: 124
                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                 STREET:
CITY: I
STATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                   State
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                                                                                                                                               October 13, 1995
                                                                                                                                                                                                 October 11,
                                                                                                                                                                                                                                                                                                                                                                                                    Street
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                                                                                                            er 13, 1995
60/021,650
12. 1996
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∵ 11, 1996
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Pred. No. 1.2e-17;
D; Mismatches 41
                                                                                                                                                                                                                                                   Version #1.25
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RESULT 7
US-09-198-452A-1
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US-08-728-742A
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GENERAL INFORMATION:
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                                                                                                                        GENERAL INFO:
APPLICANT:
TITLE OF I
                                                                                                                                                                  Sequence 11, Application US/08728742A Patent No. 6579695
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragritte OF INVENTION: thereof and uses thereof, in particular for the diagnosis, TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 122
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                                                                               NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
   COMPUTER
                         STREET:
CITY: B
STATE:
COUNTRY:
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126 amino aci
                                                                                                                           : Ralph H. INVENTION:
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2109
READABLE
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imilarity 35.3%;
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                                          Massachusetts
                                                                     28 State
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                            USA
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                                                                                                                                                                                                                                                                                                                                                                 Score 135.5; DB 4;
Pred. No. 1.6e-09;
9; Mismatches 49;
                                                                                                                                                                                                                                                                                --APYFSQAPFS-GKIWLSISHTDQFVTASVI 115
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MEDIUM TYPE:

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Best Local S
Matches 40
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Patent No
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GENERAL IN.
APPLICANT:
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sequence 2, Application US/08728742A
sequence 1, Application US/08728742A
sequence 2, Application US/08728742A
sequence 3, Application US/08728742A
sequence 3, Application US/08728742A
sequence 3, Application US/08728742A
sequence 4, Application US/08728742A
sequence 5, Application US/0872874
                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728,742A
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                                                                                                            FILING DATE: October 11, PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ralph H. Lambalot, Am
TITLE OF INVENTION: PHOSPHOPANTE
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: E
STATE:
APPLICATION NUMBER: 60/005,152 FILING DATE: October 13, 1995 APPLICATION NUMBER: 60/021,650 FILING DATE: July 12, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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FILING DATE: October 11,
ZIOR APPLICATION DATA:
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SOFTWARE: Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Similarity 32.5%;
40; Conservative
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IBM PC compatibl
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October 13, 1995
NUMBER: 60/021,650
July 12, 1996
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c 11, 1996
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Pred. No. 1.7e-06;
2; Mismatches 40
                                                                                                                                                                                                                              Version
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USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 40
                                     APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION
TITLE OF INVENTION
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ANDRESSEE: LAHIVE & COCKFIELD, LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ralph
TITLE OF INVENTION
                                                            INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION
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SOFTWARE: PatentII
CURRENT APPLICATION I
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MOLECULE 1
FRAGMENT 1
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COMPUTER
MEDIUM
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                                                                             FILING
TOPOLOG
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY
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3, 6579695
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                                                                                                                                                                                                                                                                                                                   READABLE FORM:
TYPE: Floppy disk
R: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
          121 amino
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L--GVKSLGGGAALKDIEIVRVNKNAPAVELHGNAKKAAEEAGVTDVKVSISHDDLQAVA
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internal
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11, 1996
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Pred. No. 1.8e-06;
22; Mismatches 40;
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US-08-728-742A-1
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GENERAL I
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Best Local S
Matches 36
                                                                                                                                 Query Match
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        TELEFAX: (617)/12 ....
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE:
08-728-742A-3
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COMPUTER READABLE
MEDIUM TYPE: F:
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TITLE OF INVENTION: PH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        TOPOLOGY: 1:
                                                                                                                     Local
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CITY: |
STATE:
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                                                                                                       17.4%;
Similarity 32.3%;
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Similarity 30.3%;
%; Conservative 1
Boston
                             MGTGISKLGFQ--DLEVLNNERGAPYF
                                                  GHGIDIEELAS ĮESAVTRHEGFAKRVLTAQEMERFTSLKGRRQIEYLAGRWSAKEAFSKA
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                                                                                                                                                                                                                                                    (617)227-7400
(617)742-4214
OR SEQ ID NO: 1:
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r 11, 1996
                                                                                                         15;
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                                                                                                      Score 107.5; DB 4;
Pred. No. 5.6e-06;
5; Mismatches 52;
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Pred. No. 2.7e-06;
); Mismatches 48
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VYL TRANSFERASES
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                         -SQAPFSG--KIWLSISHTDQFVTASV
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RESULT 13
US-09-328-352-7929
; Sequence 7929, Application US/09320000
; Patent No. 6562958
; GENERAL INFORMATION;
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO INTITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
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US-08-728-742A
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Matches
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Best Local :
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FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
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COMPUTER I
MEDIUM
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CORRESPOND
ADDRESSE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: Octob
PRIOR APPLICATION DATE
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CITY: B
STATE:
COUNTRY:
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INVENTION:
F SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                17.3%; Score 107; DB 4; Imilarity 32.7%; Pred. No. 6.7e-06; Conservative 19; Mismatches 37;
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EE: LAHIVE & COCKFIELD,
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579695
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ICATION DATA:
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PHOSPHOPANTETHEINYL TRANSFERASES
78
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r 11, 1996
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RESULT 15
US-08-728-742A-8
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US-09-134-001C-3478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al; TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOST; FILE REFERENCE: GTC-007; CURRENT APPLICATION NUMBER: US/09/134,001C; CURRENT FILING DATE: 1998-08-13; PRIOR APPLICATION NUMBER: US 60/064,964; PRIOR FILING DATE: 1997-11-08; PRIOR APPLICATION NUMBER: US 60/055,779; PRIOR APPLICATION NUMBER: US 60/055,779; PRIOR FILING DATE: 1997-08-14; NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3478
LENGTH: 208
TYPE: PRT
ORGANITO
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LENGTH: 233
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Best Local S
Matches 24
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Best Local S
Matches 27
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GENERAL INFORMATION:
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                                                                                                                                            APPLICANT:
TITLE OF IN
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                TITLE OF INVENTION: PH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                             ADDRESSEE:
STREET: 28
CITY: Bost
                                                     STATE: N
COUNTRY:
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6380370
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Similarity 30.8%;
24; Conservative 19
                                                                               Boston
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PHOSPHOPANTETHEINYL TRANSFERASES
78
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Pred. No. 0.034;
15; Mismatches
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Best Local
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SEQUENCE (
LENGTH:
                                                                                                                                                                                                                                                                                                                 NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:
 completeme : 22
                                                                                                                                                                                                                                                                                            TYPE:
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internal
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Pred. No. 0.064;
7; Mismatches 3
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(c) 1993
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                                        model
; ; Search time 20 Seconds
(without alignments)
586.629 Million cell updates/sec
                                                                 5.1.6
Compugen Ltd.
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Title:
Perfect so
Sequence: US-09-897-645-1 618 1 MRMIVGHGIDIEEL

score:

MRMIVGHGIDIEELASIESA..

.ISHTDQFVTASVILEENHES 122

Scoring table: BLOSUM62

Searched: 283308 seqs, Gapop 10.0 Gapext 0.5 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum Maximum BG seq length: seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45

100% 45 Si

summaries

Database PIR pir1: *
pir2: *
pir3: * 76:*

Pred. score and is S T No. is the new greater than serived by the number number of results predicted by chance to have a n or equal to the score of the result being printed, analysis of the total score distribution.

SUMMARIES

Result

Query

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olo-[acyl-carr	7155	N	,		25.	29
lo-acyl carrier	8289	N	-		•	28
robable holo-[ac	8128	N	-		13	27
robable acyl-car	8564	N	N		35.	26
cyl-carrier prot	7209	N	N		35.	25
l-carrier prot	8653	N	N	μ,	•	24
holo-[9078	N	N	H	35.	23
Ξ,	F035	N	N	'n	37.	22
չ՝	4229	Ļ	N		39.	21
holo-[acyl-carrier	7127	N	N	Ņ	14	20
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othetic	9105	ผ	N	4.	48.	16
o-[acy]	G082	N	N	4.	49.	15
o-[acyl	8183	N	N	4.	51.	14
holo-acyl-carrier	9696	N	N	7	69.	<u>1</u> 3
othetical prot	A97810	N	131	27.7	17	12
holo-(acyl carrier	7234	Ŋ	g	7.	•	11
-[acyl-carrie	7166	N	V)	9	18	10
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lo-ACP synthas	8999	N	1	ω ·	\circ	8
lo-acvl-c	D154	N	ب	9	N	7
o-acvl-carrier	E118	N	\mathbf{H}	7.	w	თ
o-[acyl-carrie	6977	_	K)	0	(H	ហ
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ALIGNMENTS

pneumoniae (strain TIG

24-Aug-2001

T.D.; Peterson, Radune, D.; Hol son, S.; He Holtzapple

RESULT 1
H95197
H95197
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: H95197
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterscon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Peterscon, J.D.; Umayam, L.A.; White, T.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneu A;Accession: H95197
A;Scatus: preliminary
A;Accession: H95197
A;Status: preliminary
A;Residues: 1-120 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75777.1; PID:g14973193; GSPDB:GN0016
A;Experimental source: strain TIGR4
C;Gene: SP1699
C;Superfamily: holo-ACP synthase pneumoniae. B.A.; Morriso

PID:g14973193; GSPDB:GN00164; TIGR:S

60 62	3 MIVGHGIDIEELASIESAVTRHEGFAKRVLTAQEMERFTSLKGRRQIEYLAGRWSAKEAF
	Y8.4%; Score 608; DB 2; Length 120; Best Local Similarity 100.0%; Pred. No. 8.3e-56; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps

RESULT 2

D98064

holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) [imported]

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_char

C;Accession: D98064

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; E 1 Streptococcus pneumonia

02-Nov-2001

S.; DeHoff, B , P.; McAhren,

B.S.;

e, R.; LeBlanc, D.J.; Lee, L.N.; Arnold, J.; Blaszczak, L.; Burgett, (Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.
A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Status: preliminary
A; Molecule type: DNA Strain R6. Jaskunas, S.R

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RESULT 4
F83714
holo-(acyl carrier protein) synthase BH0518 [imp C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Date: 01-Dec-2000 #sequence_revision 01-Dec-20
C; Accession: F83714
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkalip
A; Reference number: A83650; MUID:20512582; PMID:
A; Accession: F83714
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-119 <STO>
A; Cross-references: GB:AP001508; GB:BA000004; NI
A; Experimental source: strain C-125
C; Genetics:
A; Gene: BH0518
C; Superfamily: holo-ACP synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acyl carrier protein synthase [imported] C; Species: Lactococcus lactis subsp. lact C; Date: 23-Mar-2001 #sequence_revision 23 C; Accession: C86730 R; Bolotin, A.; Wincker, P.; Mauger, S.; J. Genome Res. 11, 731-753, 2001
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A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: GB:AE005176; PID:g12723769;
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: acpS
C;Superfamily: holo-ACP synthase
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A;Cross-references: GB:AE007317;
C;Genetics:
A;Gene: acpS
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transfer
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A;Status: prelimina
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Similarity 100.0%;
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Flaser, P.; Frangeul, L.
Dominguez-Bernal, G.; D.
Jones, L.M.; Karst, U.
Lence 294, 849-852, 2001

L.; Buchrieser, C.; Amend, Duchaud, E.; Durand, L.;

Dussurget,

A.; Baquero, I

F.; Berche, P.; Entian, K.D.;

P.;

; Bloeck Fsihi,

#text_change

14-Dec-2001

[imported]

Listeria

monocytogenes

cience

R;Glaser,

AE1185

holo-acyl-carrier protein synthase homolog lmo0885 C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 C;Accession: AE1185

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A; Gene: ydcB
C; Superfamily:
C; Keywords: coe
                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; t
A; Molecule type: DNA
A; Residues: 1-121 < KUN>
A; Cross-references: GB: Z99106; GB: AL009126; NID: g2632653;
A; Experimental source: strain 168
C; Gene: ydcB
C; Superfaces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_C;Accession: H69772
R;Kunst, F.; Ogasawara, N.; Moszon -
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A; Authors: Fou
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%imilarity 52.6%;
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                                                                                                                                                                                                                                                                                                                                                      holo-ACP
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                                                                                                                                                                                                                                                             40.6%; Score 251; DB 1 larity 44.6%; Pred. No. 8e-19; Conservative 25; Mismatches
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illet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
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transferase
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RESULT 8
E89999
holo-ACP synthase [imported] - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-7
C;Accession: E89999
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Babama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sachiha, Phiha, T.; Hattori, M.; Ogasawara, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD1543
holo-acyl-carrier protein syntn
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_r
C-accession: AD1543
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, J., Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J., A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1543
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A; Experimental source: strain Clip11262
C; Genetics:
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A; Cross-references: GB:NC 003210;
A; Experimental source: strain EGD-C; Genetics:
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C; Superfamily:
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A; Residues: 1-11
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C;Superfamily:
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1185
A;Status: preliminary
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A; Residues: 1-11
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Pred. No. 5.7e-17;
30; Mismatches 35;
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Pred. No. 1.9e-16;
Pred. Mismatches 36;
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                                                        Baba,
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                         aba, T.; Yuzawa, H.; Kobayas
Sawano, T.; Inoue, R.; Kait
N.; Hayashi, H.; Hiramatsu,
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R.; Kaito, C.; Sekimizu,
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; Entian, K.I
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Voss, H.; Wehland
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Voss, H.; Wehland
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A; Gene: VC2457
A; Map position:
C; Superfamily:
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C;Species: Vibr
C;Date: 18-Aug-
C;Accession: F8
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A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
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A; Residues: 1-126 < HEI >
A; Cross-references: GB: AE004316;
A; Experimental source: serogroup
C; Genetics:
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A;Status: preli
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A; Residues: 1-119 < KUR>
A; Cross-references: GB: BA000018; PID: g13701866;
A; Experimental source: strain N315
C; Genetics:
A; Gene: dpj
C; Superfamily: holo-ACP synthase
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A;Title: Whole genome sequencing of meticillin-resistant
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89999
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Vibrio cholerae
-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
1: F82072
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                              FSKALGTGLGKHVAFNDIDCYNDELGKPKIDYEGFI--VHVSISHTEHYAMSQVVLEKS 117
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holo-ACP
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                                                                                                                                                                   30.3%; Score 187.5; DB 2; larity 40.3%; Pred. No. 3.2e-12; Conservative 23; Mismatches 35;
                                                                                                                                                                                                                                         synthase
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                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:BAB43158.1; GSPDB:GN00149
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N1696

RESULT 10

F71662
holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) RP577 - C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_C;Accession: F71662
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; S

Sicheritz-Ponten,

H

Alsmark,

_change

03-Nov-2000

Rickettsia

116

YAMATVILE

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RESULT 11
B72345
holo-(acyl carrier protein) synt
C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_re
C; Accession: B72345
R; Nelson, K.E.; Clayton, R.A.; G
Garrett, M.M.; Stewart, A.M.; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 396, 133-140, 1998
A; Title: The genome sequence o
A; Reference number: A71630; MU
A; Accession: F71662
A; Status: preliminary; nucleic
A; Molecule type: DNA
A; Residues: 1-126 < AND>
A; Cross-references: GB: AJ23527
A; Experimental source: strain
C; Genetics:
A; Gene: acpS; RP577
C; Superfamily: holo-ACP syntha
C; Keywords: coenzyme A; transf
   RESULT 12
A97810
hypothetical
C;Species: R
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A;Molecule type: DNA
A;Residues: 1-169 <ARN>
A;Cross-references: GB:AE001741; GB:AE000512;
A;Experimental source: strain MSB8
C;Genetics:
C;Genetics:
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Similarity 38.4%;
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..M.; Cotton,
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MUID:99287316;
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MUID:99039499;
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Pred.
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Pred. No. 1.5e-11;
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red. No. 1.6e-10;
Mismatches 30;
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-20 C;Accession: A97810
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia pro A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: A97810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03419.1; PID:g15619986; GSPDB:GN C;Genetics:
A;Gene: acpS
C;Superfamily: holo-ACP synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Sola;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96960
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78469.1; PID:g15023
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A:Gene. Cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            holo-acyl-carrier protein synthase [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Accession: B96960 R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
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C;Superfamily:
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Pred. No. 1.7e-
31; Mismatches
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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: D81833
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81833
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <PAR>
A;Cross references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85252.1; PID:g738066
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: acpS; NMA2033
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transferase
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-126 < PAR>
A; Cross-references: GB: AL513382; P: C; Genetics:
A; Gene: STY2823
C; Superfamily: holo-ACP synthase C; Keywords: coenzyme A; transferasi
                                                                                                                                                                                                                                                                                                                                                                                               R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dovies, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0828
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pick
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                                                                                                                                                                                                                                                                                                                           PIDN: CAD02779.1;
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Davis, P.; Davies, R.M.; Dowd,
                              RIWGEALTLAEKLGVAHMHVTLAD
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Search completed: December 10, 2003, 19:36:56 Job time : 21 secs

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Run on: December 10, 2003, 19:32:01 ; Search time 13 Seconds (without alignments)
441.328 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-897-645-1 618 1 MRMIVGHGIDIEELASIESA..ISHTDQFVTASVILEENHES 122

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: Searched: 127863 seqs, 47026705 residues 127863

Minimum Maximum BG BG seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RT RN RN	RA RA RA RA	RA R	RR	RESULT ACPS ST ID AC AC QU AC QU DT 21
ome acte	SEQUENCE FROM N.A. STRAIN=ATCC BAA-255 / R6; MEDLINE=21429245; PubMed=11544234; Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu DJ., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun PM., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L., Glass J.I.;	SEQUENCE FROM N.A. STRAIN=ATCC BAA-334 / TIGR4; MEDLINB=21357209; PubMed=11463916; Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."; Science 293:498-506(2001).	SP1699 OR SPRIS41. occus pneumoniae, and occus pneumoniae (strain ATC); Firmicutes; Lactobacillale; occus. ID=1313, 171101; FROM N.A. ICC BAA-255 / R6; 20469436; PubMed=10903317; er K.A., Peery R.B., Meier T. ical and molecular analyses crier protein synthase, an enzesis."; Chem. 275:30864-30872(2000).	1 TRPN CPS_STRPN STA 9F7T5; 8-FEB-2003 (Rel. 8-FEB-2003 (Rel. 8-FEB-2003 (Rel. 10-[acyl-carrier 1'-phosphopanteth

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ACPS STRMU
ID ACPS STRMU STANDARD; PRT; 119 AA.
AC Q8DSF3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)
DE (4'-phosphopantetheinyl transferase acpS).
GN ACPS OR SMU.1835.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococus.
OX NCBI_TaxID=1309;
RN [1]
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DR EMBL; AE007463; AAK75777.1; -.

PIR; D98064; D98064.

DR PIR; H95197; H95197.

DR PDB; 1FTE; 12-SEP-01.

DR PDB; 1FTH; 12-SEP-01.

DR PDB; 1FTH; 12-SEP-01.

PR HAMAP; MF_00101; -; 1.

IN InterPro; IPR002582; ACPS.

IR Pfam; PF01648; ACPS; 1.

R ProDom; PD004282; ACPS; 1.

R TIGRFAMS; TIGR00556; pantethn_tr

TIGRFAMS; TIGR00556; pantethn_tr

Transferase; Lipid synthesis; Far

3D-structure; Complete proteome.

METAL 8

METAL 58

MAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Transfers the 4'-phosphopantetheine moiety A to a Ser of acyl-carrier protein (By similarity). CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] 3',5'-bisphosphate + holo-[acyl-carrier protein]. COFACTOR: Magnesium (By similarity). SUBUNIT: Homotrimer. SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFIFMANTY.
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MAGNESIUM (BY SIMILARITY).

388 MW; 7FFB1848AC63DAEE CRC64;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)
(4'-phosphopantetheinyl transferase acps).
ACPS OR SPYM3_1564 OR SPS0303 OR SPYM18_1872.
Streptococcus pyogenes (serotype M3), and
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococc
SEQUENCE FROM N.A. STRAIN=MGAS315 / Se MEDLINE=22133808; F Beres S.B., Sylva G Mammarella N.D., Li Campbell D.S., Smit
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Pfam; PF01648; ACPS; 1.

ProDom; PD004282; ACPS; 1.

TIGRFAMs; TIGR00516; acpS; 1.

TIGRFAMs; TIGR00556; pantethn trn; 1.

Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium; Complete proteome.

METAL 8 8 MAGNESIUM (BY SIMILARITY).
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MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
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Similarity 62.7%; Pred. No. 7e-33;
74; Conservative 24; Mismatches
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A159 /
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FION: Transfers the 4'-phosphopantetheine moiety from a Ser of acyl-carrier protein (By similarity).

LYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = aderology and a ser of acyl-carrier protein] = aderology and a ser of acyl-carrier protein].

TOR: Magnesium (By similarity).

ELULAR LOCATION: Cytoplasmic (By similarity).

LARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY.
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AS315 / Serotype M3; 2133808; PubMed=12122206; 1., Sylva G.L., Barbian K.D., a N.D., Liu M.-Y., Smoot J.C. D.S., Smith T.M., McCormick C

J.K.,

Lei B., Hoff J.S.,
, Porcella S.F., Parkins
J.K., Leung D.Y.M.,

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Proc. Natl. Acad [2]
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EMBL; AP005142; BAC63398.1; -
EMBL; AE010093; AAL98380.1; -
HAMAP; MF_00101; -; 1.
InterPro; IPR002582; ACPS.
InterPro; IPR004568; Pantethn
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS; 1.
TIGRFAMs; TIGR00516; acpS; 1.
TIGRFAMs; TIGR00556; pantethn
Transferase; Lipid synthesis;
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"The genome of invasive Streptococcus pyogenes; of S. pyogenes SSI-1, SF370 and MGAS8232."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ days
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STRAIN=SF370 / ATCC 700294 / Serotype M1;

MEDLINE=21192684; PubMed=11296296;

A Primeaux C., Sezate S., Suvorov A.N., Savic D.J., Lin S.P.,

A Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

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A Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

A Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Youn X., Clifton S.W., Roe B.A., McLaughlin R.,

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

C. -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme

A to a Ser of acyl-carrier protein (By similarity).

C. -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine

3',5'-bisphosphate + holo-[acyl-carrier protein].

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

C. -!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS

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TIGRFAMs; TIGR00556; pantethn_trn; 1.
Transferase; Lipid synthesis; Fatty acid biosynthesis;
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01-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
01-carrier protein synthase (EC 2.7.8.7) (Holo-ACP synthase)
03 (Rel. 41, Created)
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STRAIN=2603 V/R / Serotype V;

K MEDLINE=22222988; PubMed=12200547;

K Mariani I., Read T.D., Brettoni C., Galli G., Mariani M., Vegni F., Maion R., Raser C.M.;

K MEDLINE=22222988; PubMed=12200547;

Messelin H., Masignan W.J., Eisen J.A., Peterson M., Lewis M.R., D., Maddupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Mariani M., Vegni F., Maion R., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mo., Mo., Rappuoli R., Telford J.L., Kasper D.L., Grandi G., Raser C.M.;

R Fraser C.M.;
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EMBL; AE014268; AAN00549.1; -.
SagaList; gbs1729; -.
TIGR; SAG1685; -.
HAMAP; MF 00101; -; 1.
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS; 1.
TIGRFAMs; TIGR00516; acpS; 1.
TIGRFAMs; TIGR00556; pantethn_transferase; Lipid synthesis; Facomplete proteome.
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emerging human pathogen, serotype V Streptococcus agal
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
-!- FUNCTION: Transfers the 4'-phosphopantetheine moie
A to a Ser of acyl-carrier protein (By similarity)
-!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein]
3',5'-bisphosphate + holo-[acyl-carrier protein].
-!- COFACTOR: Magnesium (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPE
                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Streptococcus agalactiae (serotype III) Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales;
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Microbiol. 45:1499-1513(2002)
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MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- FUNCTION: Transfers the 4'-phosphopantetheine moiety fi
                                                                                                                                                                                                                                           InterPro; IPR002582; ACPS.
InterPro; IPR004568; Pantethn_trn.
InterPro; IPR004568; Pantethn_trn.
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS; 1.
TIGRFAMs; TIGR00516; acpS; 1.
TIGRFAMs; TIGR00556; pantethn_trn; 1.
Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Transfers the 4'-phosphopantetheine moiety from A to a Ser of acyl-carrier protein (By similarity).

CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adel 3',5'-bisphosphate + holo-[acyl-carrier protein].

COFACTOR: Magnesium (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY.

FAMILY.
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C86730; C867
AP; MF_00101;
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)03 (Rel. 41, Last annotation update)
/l-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP)
hopantetheinyl transferase acps).
                                                           MVFGTGVDNVELSRIQKALTRSERFVEQVLTAVELEKYNSFQSTARKTEFLAGRWAAKEA 60
                                                                         MIVGHGIDIEELASIESAVTRHEGFAKRVLTAQEMERFTSLKG-RRQIEYLAGRWSAKEA 61
                                                                                                                       48.9%; Score 302; DB 1; I imilarity 51.3%; Pred. No. 2.1e-23; Conservative 25; Mismatches 31;
                                                                                                                                                                                                                                  proteome.
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FSKAMGTGISKLGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEE
                            FSKAMGTGISK-LGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEEN 119
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                                                                                                                                                                                     59
119 AA;
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C86730.
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59 NW;
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MAGNESIUM (BY SIMILARITY).
; 1F57300FB4466AA9 CRC64;
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.es; Streptococcaceae;
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ACPS BACHD STANDARD; PRT; 119
Q9KFG1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence updates
28-FEB-2003 (Rel. 41, Last annotation updates)
Holo-[acyl-carrier protein] synthase (EC)
(4'-phosphopantetheinyl transferase acps
ACPS OR BH0518.
                                                                                                                                                                                                                                                                                                             PIR; F83714; F83714.

HAMAP; MF_00101; ~; 1.

InterPro; IPR002582; ACPS.

InterPro; IPR004568; Panteth
Pfam; PF01648; ACPS; 1.

ProDom; PD004282; ACPS; 1.

TIGRFAMS; TIGR00516; acpS; 1

TIGRFAMS; TIGR00556; panteth
Transferase; Lipid synthesis
                                                                                                                                                                                                                                                         METAL
METAL
SEQUENCE
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ACPS OC
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-!- FUNCTION: Transfers the 4'-phosphopantetheine moiety A to a Ser of acyl-carrier protein (By similarity).

-!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] 3',5'-bisphosphate + holo-[acyl-carrier protein].

-!- COFACTOR: Magnesium (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                            OCEIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horikoshi K.;
"Complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., S
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus halodurans.
Bacteria; Firmicutes;
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                    Complete proteome.
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               OCEIH
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                                                                                                                                                                                                   61;
                                                                                                                                                                       W
                                                                                                                                                                                                               Similarity
                                                                                 VKAVGTGISAEYGWHDLEVLSDERGKPVLS-VNLDATIHVSISHSQSYAIAQVILE
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                                                                                                            SKAMGTGIS-KLGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILE
                                                                                                                                                                      MIVGHGIDIEELASIESAVTRHEGFAKRVLTAQEMERFTSLKGRRQIEYLAGRWSAKEAF
                                                                                                                                          MIIGTGIDIVELERIQSMVEKHPRFVKKILTENEQEVFARLSRRRRLE
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119 AA;
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hilarity 52.6%;
Conservative 1
              STANDARD;
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synthesis;
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13421 MW;
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Pantethn_trn.
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Pred.
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MAGNESIUM (BY SIMILARITY).
; 2279E552549041C9 CRC64;
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                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                  acid biosynthesis;
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(EC 2.7.
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ID ACPS BACSU
AC P96618;
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DT 30-MAY-2000 (
DT 15-SEP-2003 (
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Best Local S
Matches 55
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Pfam; PF01(
ProDom; PD(
TIGRFAMs;
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15-SEP-2003
15-SEP-2003
Holo-[acyl-c
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ACPS OR OB
                      15-SEP-2003 (Rel. 39, Last sequence update)
Holo-[acyl-carrier protein] synthase (EC 2.
(4'-phosphopantetheinyl transferase acpS).
Bacillus subtilis
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METAL
SEQUENCE
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MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-HTE831 / DO
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NCBI_TaxID=182710;
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FUNCTION: Transfers the 4'-phosphopantetheine moiety from A to a Ser of acyl-carrier protein (By similarity).

CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adel 3',5'-bisphosphate + holo-[acyl-carrier protein].

COFACTOR: Magnesium (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY.
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s; TIGR00516; acpS; 1.
s; TIGR00556; pantethn_trn; 1
rase; Lipid synthesis; Fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation - pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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03 (Rel. 42, Last sequence update)
03 (Rel. 42, Last annotation update)
1-carrier protein] synthase (EC 2.7.8.7)
nopantetheinyl transferase acps).
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119 AA;
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                                                                                                                                                 STANDARD;
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58 M
13474 MW;
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Pred. No. 4.7e-21;
26; Mismatches 34
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MAGNESIUM (BY SIMILARITY).
; 2AF757EEAEA574DE CRC64;
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Bacteria; NCBI_TaxII

Firmicutes;

Bacillales; Bacillaceae;

Bacillus

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Reprise R., Boursier L., Brans A., Braum M., Brignell S.C., Brons S., Brons A., Broullet S.C., Brons S., Brons M., Brignell S.C., Brons S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Coloi S.K., Codami J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D., Emmerson P.T., Entit R. C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Dudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Seklguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Seklguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K., A., Takeuchi M., Vandenbol M., Vannier F., Vassarotti A., Vandenbol M., Vannier F., Vassarotti A., The Schikawa H., Danchin A., Tosalo V., With Complete Genome sequence of the Gram-nositive bacteries Bacillus Complete Genome sequence of the Gram-nositive bacteries Bacillus Complete Genome sequence of the Gram-nositive bacteries Bacillus C., Schikawa H., Danchin A., Take Gram Deniza C., Schikawa H., Danchin A., Sentin G., Schikawa H., Danchin A., Sentin G., Schikawa H., Danchin A., Schikawa H., Danchin A., Sentin G., Schikawa H., Danchin A., Schik
                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the Gram-positive bac subtilis.";
Nature 390:249-256(1997).

-!- FUNCTION: Transfers the 4'-phosphopantetheine moie A to a Ser of acyl-carrier protein (By similarity).

-!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein 3',5'-bisphosphate + holo-[acyl-carrier protein].

-!- COFACTOR: Magnesium (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPE.
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SEQUENCE FROSTRAIN=168;
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MEDLINE=98044033;
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ra N., Moszer I., i
ro M.G., Bessieres
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puano V., Carter N.M.,
mings N.J., Daniel R.A.,
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EMBL; AB001488; BAA19299.1; -EMBL; Z99106; CAB12269.1; -PIR; H69772; H69772.

PDB; 1F7L; 27-JUN-01.

PDB; 1F80; 15-MAY-02.

SubtiList; BG12089; acps.

HAMAP; MF_00101; -; 1.

InterPro; IPR002582; ACPS.

InterPro; IPR004568; Pantethn
Pfam; PF01648; ACPS; 1. ProDom; PI TIGREAMS; TIGREAMS; ## PD004282; ACPS; 1.

MS; TIGR00516; acpS;

MS; TIGR00556; pantati pantethn_trn; ACPS. Pantethn trn

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03 (Rel. 41, Last sequence update)
03 (Rel. 41, Last annotation update)
1-carrier protein] synthase (EC 2.7.
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Pred. No. 2.7e-18;
25; Mismatches 32
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RX MEDLINE-21537279; PubMed=11679669;
RA Baquero F., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Ra Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Domann E., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell F.
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
R Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
T "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
C -I- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coen
A to a Ser of acyl-carrier protein (By similarity).
-!- COFACTOR: Magnesium (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

40-[acyl-carrier protein] synthase (EC 2.7.8)

(4'-phosphopantetheinyl transferase acps).

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TIGREAMS; TIGR00516; acpS; 1.
TIGRFAMS; TIGR00556; pantethn_t
Transferase; Lipid synthesis; F
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METAL 8 8 MA
METAL 58 58 MA
SEQUENCE 118 AA; 13257 MW;
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InterPro; IPR002582; ACP;
InterPro; IPR004568; Pani
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS;
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Bacteria; Firmicutes;
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       s SWISS-PROT entry is copyright. It is p
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by non-profit institutions as long
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ities requires a license agreement (See
send an email to license@isb-sib.ch).
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ed. No. 1.6e-16;
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RESULT 12
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SEQUENCE |
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28-FEB-2003 (Rel. 41, Last annotation update)
Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)
(4'-phosphopantetheinyl transferase acps).
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                                                                                                                                                                                                            Europe
                                                                                                                                                                                                                                                                                      FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenz A to a Ser of acyl-carrier protein (By similarity). CATALYTIC ACTIVITY: COA + apo-[acyl-carrier protein] = adenosin 3',5'-bisphosphate + holo-[acyl-carrier protein]. COFACTOR: Magnesium (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS FAMILY.
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o; IPR004568; Pantethn_trn.
F01648; ACPS; 1.
PD004282; ACPS; 1.
s; TIGR00516; acpS; 1.
s; TIGR00556; pantethn_trn; 1.
rase; Lipid synthesis; Fatty acid biosynthesis;
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543; AD1543.
t; LIN00884;
                                                                                                                                A., Griffin H., Gasson M.J.; and characterisation of an alanine racemase
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118 AA;
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                                                                                                                                                                                    ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this in the content is in the content in the content in the content is in the content in the content in the content is in the content in the conte
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                                                                                                                              license agreement (
license@isb-sib.ch)
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InterPro; InterPro; Pfam; PF0]

1PR002582; IPR004568;

ACPS

ACPS; 1. 32; ACPS; 1.

Pantethn

EMBL; !

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78312; CAC03496.1;

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C STRAIN=NCTC 8325;

X MEDLINE=98434453; PubMed=9756984;

Y Sequence of the putative alanine racemase operon in Staphylococcus

T aureus: insertional interruption of this operon reduces D-alanine

T aureus: insertional interruption of this operon in Staphylococcus

T aureus: insertional interruption of this operon reduces D-alanine

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InterPro; IPR002582; ACPS.
InterPro; IPR004568; Pantet
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS; 1.
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30-MAY-2000
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TIGRFAMS; TIG
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30-MAY-2000 (Rel. 39, Last sequence 1
28-FEB-2003 (Rel. 41, Last annotation
Holo-[acyl-carrier protein] synthase (4'-phosphopantetheinyl transferase a
ACPS OR DPJ.
                                                                                                                                                                                                                                                                                                                                                                 between
the Euro
                                                                                                                                                                                                                                                                                     modified and this statement is not entities requires a license agreement or send an email to license@isb-sil
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European Bioinformatics Institute. The
by non-profit institutions as long
by non-profit institutions as long
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TaxID=1280;
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se; Lipid synthesis;
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                                Fatty acid biosynthesis;
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MAGNESIUM (BY SIMILARITY)
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Choy H.E.,
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Holo-[acyl-carrier protein] synthase (EC 2.7.
(4'-phosphopantetheinyl transferase acps).
ACPS OR VV11569.
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15-SEP-
15-SEP-
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Dom; PD004282; ACPS; 1.
RFAMs; TIGR00516; acpS; 1.
RFAMs; TIGR00556; pantethn trn; 1.
1sferase; Lipid synthesis; Fatty aciolete proteome.
                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                             nitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

FUNCTION: Transfers the 4'-phosphopantetheine moiety from a to a Ser of acyl-carrier protein (By similarity).

CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = ader 3',5'-bisphosphate + holo-[acyl-carrier protein].

COFACTOR: Magnesium (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY.
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SKAMGTGISK-LGFQDLEVLNNERGAPYFSQAPFSGKI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome
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126 AA;
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                                                                                             34.1%;
llarity 42.4%;
Conservative 22
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58 N
13633 MW;
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Pred. No. 3.1e-
2; Mismatches
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MAGNESIUM (BY SIMILARITY).
80BDE9222F04E78E CRC64;
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ACPS STAAM STANDARD; PRT; LL7 ....

Q99SI4;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update)

40-[acyl-carrier protein] synthase (EC 2.7.8.7) (Ho

41-phosphopantetheinyl transferase acps).

ACPS OR DPJ OR SAV2071 OR SA1875 OR MW1995.

ACPS OR DPJ OR SAV2071 OR SA1875 OR MW1995, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Mu50 / ATCC 700699, and N315;

KMEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., I
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., ]

Kanamori M., Matsumaru H., Maruyama A., Murakami H., I
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I.
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshi
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staph
aureus.";
EMBL; AP003364; BAB58233.1;
EMBL; AP003136; BAB43158.1;
EMBL; AP004829; BAB95860.1;
PIR; E89999; E89999.
HAMAP; MF_00101; -; 1.
InterPro; IPR002582; ACPS.
InterPro; IPR004568; Pantet
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS; 1.
TIGRFAMs; TIGR00556; pantet
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Baba T., Takeuchi
Nagai Y., Iwama N.
Yamamoto K., Hiram
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a copyrement the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       acquired MRSA.";
Lancet 359:1819-1827(2002).

-!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from A to a Ser of acyl-carrier protein (By similarity).

-!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = ade:
3',5'-bisphosphate + holo-[acyl-carrier protein].

-!- COFACTOR: Magnesium (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto K., Hiramacsu K.,
"Genome and virulence determinants
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Pakeuchi F., Kuroda M., Yuzawa
Iwama N., Asano K., Naimi T.,
C., Hiramatsu K.;
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BAB43158.1;
BAB95860.1;
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                                             FSKALGTGLGKHVAFNDIDCYNDELGKPKIDYEGFI--VHVSISHTEHYAMSQVVLEKS 117
                                                                                            33.7%; Score 208; DB 1; Length 119; imilarity 37.8%; Pred. No. 5.2e-14; Conservative 29; Mismatches 41; Indels
                                                                                                                                                                      use; Lipid synthesis; Fatty acid biosynthesis; Magnesium; proteome.

8 MAGNESIUM (BY SIMILARITY).
              FSKAMGTGISK-LGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEEN 119
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119 AA;
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59
13634 MW;
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MAGNESIUM (BY SIMILARITY).
; E2EF3C5A696E7DD2 CRC64;
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Search completed: December 10, 2003, 19:35:35
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2: sp_bac

3: sp_fun

4: sp_hum

5: sp_inv

6: sp_mam

7: sp_mam

7: sp_org

9: sp_org

10: sp_vi

11: sp_vi

13: sp_vi

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Q8dc72 vibrio vuln
Q8dc72 vibrio vuln
Q8cnk6 staphylococ
Q8d303 wiggleswort
Q8mnp2 dictyosteli
Q8eh77 shewanella
Q8ff19 escherichia
P78615 emericella
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STRAIN=2603 V/R / Serotype V;

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STRAIN=NEM316 / Serotype III;
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
Claser P., Rusniok C., Buchrieser C.
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L-MAR-2003 (TrEMBLrel. 23, L
Holo-(acyl-carrier-protein) s
ACPS OR SAG1685.
Streptococcus agalact
Bacteria; p.
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"Genome sequence of Streptococcus aginvasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766852; CAD47388.1; -.
SagaList; gbs1729; -.
Hypothetical protein; Complete prote
SEQUENCE 119 AA; 13268 MW; COEEB
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SEQUENCE FROM N.A.
STRAIN=NCIMB8826;
MEDLINE=97315262; PubMed=9171436;
Hols P., Defrenne C., Ferain T., De
"The alanine racemase gene is essen
                                                                                                                                                                                         Hypothetical 8.0 kDa protein (Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobac:Lactobacillus.
NCBI_TaxID=1590;
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E831 / DSM 14371 / JCM 11309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MICGVGIDIIELNRMEALIERNERFIERILTENEQRKFQRLSANRKVEYIAGRFAAKEAF
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Firmicutes; Bacillales;
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synthase.
                         f., Derzelle S., Delplace
essential for growth of )
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RESULT
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STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.
Choy H.E.;
"Complete genome sequence of
Submitted (DEC-2002) to the E
EMBL; AE016802; AA009993.1; -
Transferase; Complete proteom
SEQUENCE 126 AA; 13633 MW;
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EMBL; Y08941; CAA70142.1;
HSSP; Q9F7T5; 1FTH.
InterPro; IPR002582; ACPS
InterPro; IPR004568; Pant
Pfam; PF01648; ACPS; 1.
ProDom; PD004282; ACPS; 1
Q8CNK6;
Q8CNK6;
01-MAR-2003
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Holo-ACP syn
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Vibrionaceae; Vibrio.
NCBI_TaxID=672;
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NON TER 1
SEQUENCE 74 AA; 80
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Pred. No. 1.7e
4; Mismatches
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RESULT 9
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Nat. Genet. 32:402-407(2002).
EMBL; AB063521; BAC24344.1; -.
Complete proteome.
SEQUENCE 120
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Q1-MAR-2003 (TrEMBLrel. 23, L
Acps protein.
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SEQUENCE P
STRAIN=ATC
Zhang Y.,
Chen Z., Y
Submitted
EMBL; AE01
Complete P
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Numan L., Yamashita A., Watanabe H.,
                                                                                                                                                                                                                                                                              NCBI
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
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Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales;
NCBI_TaxID=1282;
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e proteome.
3 117 AA; 13535 MW;
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TCC 12228;
, Ren S., Li H.,
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ACATVIFEDN
                                    <u>ĖAASKĀFĢLĠMKKGLYFSQFEVLNNNLGKPYFKFNNTAKNLIKĀLNITNIHLSLTDERKY</u>
                                                                            VTASVILEEN 119
                                                           EAFSKAMGTGISK-LGFQDLEVLNNERGAPYFS-
                                                                                          IVGHGIDIEELASIESAVTRH-EGFAKRVLTAQEMERFTSLKGRRQ---IEYLAGRWSAK
                                                                                                                                 imilarity
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                                                                                                                     28.5%; Score 176; DB 16; larity 36.2%; Pred. No. 2.2e-10; Conservative 23; Mismatches 46;
132
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RESULT 10
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RP SEQUE
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RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
DR TIGR; SO1352; -.
CW Complete proteome.
127 AA: 1260.
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NCBI TaxID=44689;
[1]
SEQUENCE FROM N.A.
STRAIN=AX4;
Gloeckner G., Eichinger L., Szafranski K.
Lehmann R., Baumgart C., Parra G., April
Tunggal B., Cox E., Quail M.A., Platzer N
"Sequence and Analysis of The
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InterPro; IPR004568; Pantethn_trn.
ProDom; PD004282; ACPS; 1.
TIGRFAMS; TIGR00516; acpS; 1.
TIGRFAMS; TIGR00556; pantethn_trn; 1.
Hypothetical protein.
SEQUENCE 158 AA; 17931 MW; A4E56FBF387B08EB
                                                                                                                                                                                                                               Bacteria; Proteobacteria; G
Alteromonadaceae; Shewanell
NCBI_TaxID=70863;
[1]
SEQUENCE FROM N.A.
STRAIN=MR-1;
MEDLINE=22297686; PubMed=12
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01-OCT-2002 (TrEMBLrel. 22
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rra G., April J.F., Guigo R., K
.A., Platzer M., Rosenthal A., l
hromosome 2 of Dictyostelium.";
EMBL/GenBank/DDBJ databases.
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Similarity 31.8%; Pred. No. 1.3e-07;
2; Conservative 25; Mismatches 38
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22388234; PubMed=12471157;
A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud
.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
.L.T., Donnenberg M.S., Blattner F.R.;
ve mosaic structure revealed by the complete genome sequenthogenic Escherichia coli.";
tl. Acad. Sci. U.S.A. 99:17020-17024(2002).
016764; AAN81536.1; -.
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R InterPro; IPR004568; Pantethn_trn.

R InterPro; IPR004568; Pantethn_trn.

Pfam; PF01648; ACPS; 1.

Pfam; PF00109; ketoacyl-synt; 1.

Pfam; PF02801; ketoacyl-synt_C; 1.

ProDom; PD004282; ACPS; 1.

TIGRFAMs; TIGR00556; pantethn_trn; 1.

PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.

Transferase.

SEQUENCE 1858 AA: 200701
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Best Loc
Matches
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Brown D.W., Adams T.H., Keller N.P.;
"Aspergillus has distinct fatty acid sy
secondary metabolism.";
Proc. Natl. Acad. Sci. U.S.A. 93:14873.
EMBL; U75347; AAB41493.1; -.
HSSP; Q9F7T5; 1FTF.
InterPro; IPR002582; ACPS.
                                                                                                                                       EMBL; AE011490; AAN50500.1; Transferase; Complete proteom SEQUENCE 126
                                                                                                                                                                                                                                                                              Q8F136;
Q8F136;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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SEQUENCE FROM
STRAIN=56601
Ren S.;
                                                                                                                                                                                                                          Leptospira interrogans.
Bacteria; Spirochaetes;
NCBI_TaxID=173;
                                                                                                                                                                                                                                                           Phosphopantetheinyl ACPS OR LA3302.
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Eurotiales; Trichocomaceae; I
NCBI_TaxID=162425;
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Similarity 34.2%;
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GVDVE---
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                                                                                                                                                                                              FROM N.A.
5601 / Serogroup
                  EAFIKAIEPGDHVILDMREIELFGKEFGKKELVLHGKSKELFLTKGYSG-CSVSISHAEN
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FVTASVIL
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116
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cel. 23, Last sequence upicel. 23, Last annotation
transferase (EC 2.7.8.7)
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14419 MW;
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                                                                                                            Score
Pred.
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Pred. No. 0.00071;
Mismatches 45
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                                                                                                    Mismatches
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                                                                                                             114.5;
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Yoshioka S
"Identific
CDNAs.";
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01-JAN-1998
01-JAN-1998
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SEQUENCE F
STRAIN=PR7
MEDLINE=98
                                                                                                 Schizosacc
Schizosacc
NCBI_TaxII
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown protein (Fragment).
Schizosaccharomyces nombo
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P78866;
01-MAY-199
01-JAN-199
01-MAR-200
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TIGRFAMs;
Transferas
SEQUENCE
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Stuible H.P., Meier S., Schweizer E.;
"Identification, isolation and biochemical characterization of
phosphopantetheine:protein transferase that activates the two t
fatty synthases of Brevibacterium ammoniagenes.";
Eur. J. Biochem. 248:481-487(1997).
EMBL; Y15081; CAA75358.1; -.
HSSP; Q9F7T5; 1FTF.
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Pfam; PF01648; ACPS; 1.
TIGRFAMs; TIGR00556; pantethn_trn; 1.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1697;
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YSTAVVVL
                               8162722; PubMed=9501991;
S., Kato K., Nakai K., Okayama
cation of open reading frames
                                                                                                                       charomyces pombe (Fission yeast).
; Fungi; Ascomycota; Schizosaccharomycetes;
charomycetales; Schizosaccharomycetaceae;
4:363-369(1997).
216; BAA13877.1;
                                                                             FROM N.A.
                                                                                                   charomyces.
D=4896;
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thiene protein transferase, Ppt1p.
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                                         Okayama H.,
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                                Schizosaccharomyces
                                            Nojima H.;
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                                                                                  Query Match 17.3%; Score 107; DB 3; Best Local Similarity 32.7%; Pred. No. 0.011; Matches 37; Conservative 19; Mismatches 37
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                                                       -GISGKGAAAPLKDIEIISSESGAPEVVLHGEAAKAATTAGVKSVSVSISHDD 366
                                         TGISKLG--
                                        --FQDLEVLNNERGAPYF--
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       2003,
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                                      -SQAPFSG--KIWLSISHTD 107
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